



PCT09

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/913,728

DATE: 01/22/2002

TIME: 10:30:33

Input Set : A:\84335143.app

Output Set: N:\CRF3\01182002\I913728.raw

3 <110> APPLICANT: KITAMURA, TOSHIO  
 4 FUJIO, KEISHI  
 6 <120> TITLE OF INVENTION: CYTOKINE RECEPTOR-LIKE PROTEINS  
 8 <130> FILE REFERENCE: 084335/0143  
 10 <140> CURRENT APPLICATION NUMBER: 09/913,728  
 C--> 11 <141> CURRENT FILING DATE: 2001-12-17  
 13 <150> PRIOR APPLICATION NUMBER: JP 1999-041936  
 14 <151> PRIOR FILING DATE: 1999-02-19  
 16 <160> NUMBER OF SEQ ID NOS: 34  
 18 <170> SOFTWARE: PatentIn Ver. 2.1  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 1278  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Mus musculus  
 25 <220> FEATURE:  
 26 <221> NAME/KEY: CDS  
 27 <222> LOCATION: (59)..(1135)  
 29 <400> SEQUENCE: 1

30	accggctcgg accgaaccag ctgtcaatca ctgcagcgtc cgcggcccg cggcgac	58
32	atg gca tgg gca ctc gcg gtc atc ctc ctg cct cgg ctc ctt acg gcg	106
33	Met Ala Trp Ala Leu Ala Val Ile Leu Leu Pro Arg Leu Leu Thr Ala	
34	1 5 10 15	
36	gca gcg gcg gcg gcg gtg acg tca cgg ggt gat gtc aca gtc gtc	154
37	Ala Ala Ala Ala Ala Val Thr Ser Arg Gly Asp Val Thr Val Val	
38	20 25 30	
40	tgc cat gac ctg gag acg gtg gag gtc acg tgg ggc tgc ggc ccc gac	202
41	Cys His Asp Leu Glu Thr Val Glu Val Thr Trp Gly Ser Gly Pro Asp	
42	35 40 45	
44	cac cac ggc gcc aac ttg agc ctg gag ttc cgt tat ggt act ggc gcc	250
45	His His Gly Ala Asn Leu Ser Leu Glu Phe Arg Tyr Gly Thr Gly Ala	
46	50 55 60	
48	ctg caa ccc tgc ccg cga tat ttc ctg tcc ggc gct ggt gtc act tcc	298
49	Leu Gln Pro Cys Pro Arg Tyr Phe Leu Ser Gly Ala Gly Val Thr Ser	
50	65 70 75 80	
52	ggg tgc atc ctc ccc gcg gcg agg gcg ggg ctg ctg gag ctg gca ctg	346
53	Gly Cys Ile Leu Pro Ala Ala Arg Ala Gly Leu Leu Glu Leu Ala Leu	
54	85 90 95	
56	cgc gac gga ggc ggg gcc atg gtg ttt aag gct agg cag cgc gcg tcc	394
57	Arg Asp Gly Gly Gly Ala Met Val Phe Lys Ala Arg Gln Arg Ala Ser	
58	100 105 110	
60	gcc tgg ctg aag ccc cgc cca cct tgg aat gtg acg ctg ctc tgg aca	442
61	Ala Trp Leu Lys Pro Arg Pro Pro Trp Asn Val Thr Leu Leu Trp Thr	
62	115 120 125	

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64 cca gac ggg gac gtg act gtc tcc tgg cct gcc cac tcc tac ctg ggc 490
65 Pro Asp Gly Asp Val Thr Val Ser Trp Pro Ala His Ser Tyr Leu Gly
66 130 135 140
68 ctg gac tac gag gtg cag cac cgg gag agc aat gac gat gag gac gcc 538
69 Leu Asp Tyr Glu Val Gln His Arg Glu Ser Asn Asp Asp Glu Asp Ala
70 145 150 155 160
72 tgg cag acg acc tca ggg ccc tgc tgt gac ttg aca gtg ggc ggg ctc 586
73 Trp Gln Thr Thr Ser Gly Pro Cys Cys Asp Leu Thr Val Gly Gly Leu
74 165 170 175
76 gac ccc gcg cgc tgc tat gac ttc cgg gtt cgg gcg tgg ccc cgg gcc 634
77 Asp Pro Ala Arg Cys Tyr Asp Phe Arg Val Arg Ala Ser Pro Arg Ala
78 180 185 190
80 gcg cac tat ggc ctg gag gcg cag cct agc gag tgg aca gcg gtg aca 682
81 Ala His Tyr Gly Leu Glu Ala Gln Pro Ser Glu Trp Thr Ala Val Thr
82 195 200 205
84 agg ctt tcc ggg gca gca tcc gcg gcc tcc tgt acc gca agc ccc gcc 730
85 Arg Leu Ser Gly Ala Ala Ser Ala Ala Ser Cys Thr Ala Ser Pro Ala
86 210 215 220
88 cca tcc ccg gcc ctg gcc ccg ccc ctc ctg ccc ctg ggc tgc ggc cta 778
89 Pro Ser Pro Ala Leu Ala Pro Pro Leu Leu Pro Leu Gly Cys Gly Leu
90 225 230 235 240
92 gca gcg ctg ctg aca ctg tcc ctg ctc ctg gcc gcc ctg agg ctt cgc 826
93 Ala Ala Leu Leu Thr Leu Ser Leu Leu Leu Ala Ala Leu Arg Leu Arg
94 245 250 255
96 agg gtg aaa gat gcg ctg ctg ccc tgc gtc cct gac ccc agc ggc tcc 874
97 Arg Val Lys Asp Ala Leu Leu Pro Cys Val Pro Asp Pro Ser Gly Ser
98 260 265 270
100 ttc cct gga ctc ttt gag aag cat cac ggg aac ttc cag gcc tgg att 922
101 Phe Pro Gly Leu Phe Glu Lys His His Gly Asn Phe Gln Ala Trp Ile
102 275 280 285
104 gcg gac gcc cag gcc aca gcc ccg cca gcc agg acc gag gag gaa gat 970
105 Ala Asp Ala Gln Ala Thr Ala Pro Pro Ala Arg Thr Glu Glu Glu Asp
106 290 295 300
108 gac ctc atc cac ccc aag gct aag agg gtg gag ccc gag gac ggc acc 1018
109 Asp Leu Ile His Pro Lys Ala Lys Arg Val Glu Pro Glu Asp Gly Thr
110 305 310 315 320
112 tcc ctc tgc acc gtg cca agg cca ccc agc ttc gag cca agg ggg ccg 1066
113 Ser Leu Cys Thr Val Pro Arg Pro Pro Ser Phe Glu Pro Arg Gly Pro
114 325 330 335
116 gga ggc ggg gcc atg gtg tca gtg ggc ggg gcc acg ttc atg gtg ggc 1114
117 Gly Gly Gly Ala Met Val Ser Val Gly Gly Ala Thr Phe Met Val Gly
118 340 345 350
120 gac agc ggc tac atg acc ctg tgaccttgaa gtcactgccca gtctatactt 1165
121 Asp Ser Gly Tyr Met Thr Leu
122 355
124 caggctgagg tcacttccctg tcttttaaata attcaaactc acaaactcctg tgccctgtctg 1225
126 tatgcaaatg tggtcacgaa tattcaaata aaatgcaaat gctatgctaa aaa 1278
129 <210> SEQ ID NO: 2
130 <211> LENGTH: 359

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131 <212> TYPE: PRT
132 <213> ORGANISM: Mus musculus
134 <400> SEQUENCE: 2
135 Met Ala Trp Ala Leu Ala Val Ile Leu Leu Pro Arg Leu Leu Thr Ala
136 1 5 10 15
138 Ala Ala Ala Ala Ala Val Thr Ser Arg Gly Asp Val Thr Val Val
139 20 25 30
141 Cys His Asp Leu Glu Thr Val Glu Val Thr Trp Gly Ser Gly Pro Asp
142 35 40 45
144 His His Gly Ala Asn Leu Ser Leu Glu Phe Arg Tyr Gly Thr Gly Ala
145 50 55 60
147 Leu Gln Pro Cys Pro Arg Tyr Phe Leu Ser Gly Ala Gly Val Thr Ser
148 65 70 75 80
150 Gly Cys Ile Leu Pro Ala Ala Arg Ala Gly Leu Leu Glu Leu Ala Leu
151 85 90 95
153 Arg Asp Gly Gly Ala Met Val Phe Lys Ala Arg Gln Arg Ala Ser
154 100 105 110
156 Ala Trp Leu Lys Pro Arg Pro Pro Trp Asn Val Thr Leu Leu Trp Thr
157 115 120 125
159 Pro Asp Gly Asp Val Thr Val Ser Trp Pro Ala His Ser Tyr Leu Gly
160 130 135 140
162 Leu Asp Tyr Glu Val Gln His Arg Glu Ser Asn Asp Asp Glu Asp Ala
163 145 150 155 160
165 Trp Gln Thr Thr Ser Gly Pro Cys Cys Asp Leu Thr Val Gly Gly Leu
166 165 170 175
168 Asp Pro Ala Arg Cys Tyr Asp Phe Arg Val Arg Ala Ser Pro Arg Ala
169 180 185 190
171 Ala His Tyr Gly Leu Glu Ala Gln Pro Ser Glu Trp Thr Ala Val Thr
172 195 200 205
174 Arg Leu Ser Gly Ala Ala Ser Ala Ala Ser Cys Thr Ala Ser Pro Ala
175 210 215 220
177 Pro Ser Pro Ala Leu Ala Pro Pro Leu Leu Pro Leu Gly Cys Gly Leu
178 225 230 235 240
180 Ala Ala Leu Leu Thr Leu Ser Leu Leu Leu Ala Ala Leu Arg Leu Arg
181 245 250 255
183 Arg Val Lys Asp Ala Leu Leu Pro Cys Val Pro Asp Pro Ser Gly Ser
184 260 265 270
186 Phe Pro Gly Leu Phe Glu Lys His His Gly Asn Phe Gln Ala Trp Ile
187 275 280 285
189 Ala Asp Ala Gln Ala Thr Ala Pro Pro Ala Arg Thr Glu Glu Glu Asp
190 290 295 300
192 Asp Leu Ile His Pro Lys Ala Lys Arg Val Glu Pro Glu Asp Gly Thr
193 305 310 315 320
195 Ser Leu Cys Thr Val Pro Arg Pro Pro Ser Phe Glu Pro Arg Gly Pro
196 325 330 335
198 Gly Gly Gly Ala Met Val Ser Val Gly Gly Ala Thr Phe Met Val Gly
199 340 345 350
201 Asp Ser Gly Tyr Met Thr Leu
202 355

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205 <210> SEQ ID NO: 3
206 <211> LENGTH: 804
207 <212> TYPE: DNA
208 <213> ORGANISM: Mus musculus
210 <220> FEATURE:
211 <221> NAME/KEY: CDS
212 <222> LOCATION: (98)..(661)
214 <400> SEQUENCE: 3
215 cgttttcggc tctaagcggc ctgggcggcc tgcactcgga ccggctcgga ccgaaccagc 60
217 tgtcaatcac tgcagcgccc gggggccggc cggcgac atg gca tgg gca ctc gcg 115
218                                     Met Ala Trp Ala Leu Ala
219                                     1           5
221 gtc atc ctc ctg cct cgg ctc ctt acg gcg gca gcg gcg gcg gcg gcg 163
222 Val Ile Leu Leu Pro Arg Leu Leu Thr Ala Ala Ala Ala Ala Ala Ala
223                                     10          15          20
225 gtg acg tca cgg ggt gat gtc aca gtc gtc tgc cat gac ctg gag acg 211
226 Val Thr Ser Arg Gly Asp Val Thr Val Val Cys His Asp Leu Glu Thr
227                                     25          30          35
229 gtg gag gtc acg tgg ggc tgc ggc ccc gac cac cac ggc gcc aac ttg 259
230 Val Glu Val Thr Trp Gly Ser Gly Pro Asp His His Gly Ala Asn Leu
231                                     40          45          50
233 agc ctg gag ttc cgt tat ggt act ggc gcc ctg caa ccc tgc ccg cga 307
234 Ser Leu Glu Phe Arg Tyr Gly Thr Gly Ala Leu Gln Pro Cys Pro Arg
235 55                                     60          65          70
237 tat ttc ctg tcc ggc gct ggt gtc act tcc ggg tgc atc ctc ccc gcg 355
238 Tyr Phe Leu Ser Gly Ala Gly Val Thr Ser Gly Cys Ile Leu Pro Ala
239                                     75          80          85
241 gcg agg gcg ggg ctg ctg gag ctg gca ctg cgc gac gga ggc ggg gcc 403
242 Ala Arg Ala Gly Leu Leu Glu Leu Ala Leu Arg Asp Gly Gly Gly Ala
243                                     90          95          100
245 atg gtg ttt aag gct agg cag cgc gcg tcc gcc tgg ctg aag ccc cgc 451
246 Met Val Phe Lys Ala Arg Gln Arg Ala Ser Ala Trp Leu Lys Pro Arg
247                                     105         110         115
249 cca cct tgg aat gtg acg ctg ctc tgg aca cca gac ggg gac gtg act 499
250 Pro Pro Trp Asn Val Thr Leu Leu Trp Thr Pro Asp Gly Asp Val Thr
251                                     120         125         130
253 gtc tcc tgg cct gcc cac tcc tac ctg ggc ctg gac tac gag gtg cag 547
254 Val Ser Trp Pro Ala His Ser Tyr Leu Gly Leu Asp Tyr Glu Val Gln
255 135                                     140         145         150
257 cac cgg gag agc aat gac gat gag gac gcc tgg cag acg acc tca ggg 595
258 His Arg Glu Ser Asn Asp Asp Glu Asp Ala Trp Gln Thr Thr Ser Gly
259                                     155         160         165
261 ccc tgc tgt gac ttg aca gtg ggc ggg gcc acg ttc atg gtg ggc gac 643
262 Pro Cys Cys Asp Leu Thr Val Gly Gly Ala Thr Phe Met Val Gly Asp
263                                     170         175         180
265 agc ggc tac atg acc ctg tgaccttgaa gtcactgccg gtctatactt 691
266 Ser Gly Tyr Met Thr Leu
267                                     185
269 caggctgagg tcaattcctg tctttaaata attcaaactc acaaatcctg tgccctgtctg 751

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271 tatgcaaagt tggtcacgaa tattcaaata aaatgcaaat gctatgctaa aaa      804
274 <210> SEQ ID NO: 4
275 <211> LENGTH: 188
276 <212> TYPE: PRT
277 <213> ORGANISM: Mus musculus
279 <400> SEQUENCE: 4
280 Met Ala Trp Ala Leu Ala Val Ile Leu Leu Pro Arg Leu Leu Thr Ala
281   1           5           10           15
283 Ala Ala Ala Ala Ala Val Thr Ser Arg Gly Asp Val Thr Val Val
284           20           25           30
286 Cys His Asp Leu Glu Thr Val Glu Val Thr Trp Gly Ser Gly Pro Asp
287           35           40           45
289 His His Gly Ala Asn Leu Ser Leu Glu Phe Arg Tyr Gly Thr Gly Ala
290           50           55           60
292 Leu Gln Pro Cys Pro Arg Tyr Phe Leu Ser Gly Ala Gly Val Thr Ser
293   65           70           75           80
295 Gly Cys Ile Leu Pro Ala Ala Arg Ala Gly Leu Leu Glu Leu Ala Leu
296           85           90           95
298 Arg Asp Gly Gly Gly Ala Met Val Phe Lys Ala Arg Gln Arg Ala Ser
299           100          105          110
301 Ala Trp Leu Lys Pro Arg Pro Pro Trp Asn Val Thr Leu Leu Trp Thr
302           115          120          125
304 Pro Asp Gly Asp Val Thr Val Ser Trp Pro Ala His Ser Tyr Leu Gly
305           130          135          140
307 Leu Asp Tyr Glu Val Gln His Arg Glu Ser Asn Asp Asp Glu Asp Ala
308  145           150           155           160
310 Trp Gln Thr Thr Ser Gly Pro Cys Cys Asp Leu Thr Val Gly Gly Ala
311           165           170           175
313 Thr Phe Met Val Gly Asp Ser Gly Tyr Met Thr Leu
314           180           185
317 <210> SEQ ID NO: 5
318 <211> LENGTH: 19
319 <212> TYPE: DNA
320 <213> ORGANISM: Artificial Sequence
322 <220> FEATURE:
323 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
325 <400> SEQUENCE: 5
326 ggggtggac catcctcta      19
329 <210> SEQ ID NO: 6
330 <211> LENGTH: 20
331 <212> TYPE: DNA
332 <213> ORGANISM: Artificial Sequence
334 <220> FEATURE:
335 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
337 <400> SEQUENCE: 6
338 cgcgcagctg taaacggtag      20
341 <210> SEQ ID NO: 7
342 <211> LENGTH: 25
343 <212> TYPE: DNA

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/913,728

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Input Set : A:\84335143.app

Output Set: N:\CRF3\01182002\I913728.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28

L:653 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28

L:674 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29

L:677 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29

L:698 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30

L:701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30

L:722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31

L:725 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31

L:750 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32

L:753 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32

L:756 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32

L:792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34